

# SEQUENCE LISTING

<110> NOVO NORDISK A/S

<120> FAMILY 44 XYLOGLUCANASES

<130> 10017

<140>

<141>

<160> 6

<170> PatentIn Ver. 2.1

<210> 1

<211> 4059

<212> DNA

<213> Paenibacillus polymyxa

<400> 1

atgagggcga	aaaatagtag	taatcttttg	ttcaaacggt	ccaaatggct	gcctgtcgtc	60
atggcctgca	cgatgatagt	aggggggggt	ttacctgctc	cagctgtggt	tcacgggtcaa	120
acggcaaaaga	ctattactat	taaagtagat	acattcaagg	atcgtaagcc	tattagccct	180
tatatatacg	gtacaaatca	ggatttggca	ggcgatgaaa	atatggctgc	cagacgactt	240
ggtggcaacc	gaatgaccgg	atacaactgg	gaaacaaata	tgtccaatgc	aggaagtgc	300
tggcagcaat	ctagcgataa	ctatttatgc	agtaatggtg	gcctgacaca	agccgaatgt	360
gaaaagccag	gagcgggtgac	gacttcgttt	catgacgaat	cgctgaagct	tggcacttat	420
tcttttagtta	cgttgccgat	ggccggttat	gtggctaagg	atggaaacgg	aagtgtgcag	480
gaaagcgaaa	aggcccttcc	cgctcggttg	aatcaggtcg	taaaacgcaa	aaatgcaccg	540
ttccaactac	agcctgatct	gaatgacaat	cggtctatg	tggatgagtt	cgccattttt	600
ttagtgaaca	agtacggcac	tgcttcaaca	aaagcggggg	tgaaggata	tgccctcgac	660
aatgaacccg	ctctctggtc	gcatacgcac	ccaegcattc	atggtgaaaa	agtcggagcg	720
aaagagttgg	tagaccggtc	agtcagttta	tccaaagctg	tgaagcgat	tgacgcgggg	780
gcagaggttt	ttggcccggt	tctttacgga	tttggcgctc	ataaagatct	tcaaactgca	840
cctgattggg	actctgtaaa	aggcaattat	agctggttcg	tagactatta	cctggatcaa	900
atgcgcctta	gctcgcaagt	cgaaggcaag	agattgctgg	atgtattcga	cgtacactgg	960
tatcccgaag	cgatgggagg	aggcatacga	attacgaatg	aggtaggcaa	tgacgaaacg	1020
aagaaagcca	gaatgcaggc	acctgcgacc	ttgtgggacc	cgacctataa	ggaagatagt	1080
tggatcgctc	aatggaacag	cgagtttttg	cccatactac	ctcgattgaa	gcagtcgggtg	1140
gataaatatt	atccgggaac	caagctggca	atgaccgagt	atagctatgg	cggcgaaaaat	1200
gatatgtccg	gcgggattgc	gatgaccgat	gtgctgggta	tcttgggcaa	aaatgatgtt	1260
tatatggcaa	actactggaa	gctaaaggat	ggtgtcaaca	actacgttag	tgccgctttac	1320
aagctttatc	gcaattatga	cggaaaaaac	tctactttcg	gtgataccag	tgtagtgccg	1380
caaacatcgg	atattgtcaa	tagctcggtc	catgcttctg	taacgaatgc	atccgacaaa	1440
gaactgcata	tcgttgtcat	gaataaaaag	atggacagcg	cattcgacgc	ccaatttgat	1500
ctttccggcg	cgaagactta	catttccggt	aaagtatggg	ggttcgataa	aaacagctcg	1560
caaattaaag	aagcagcgcc	aatcacgcaa	atttcaggca	accgttttac	ttataccgta	1620
ccgcctttga	cggcataatca	catttgtgctg	actactggca	atgacacgtc	tccagtggaa	1680
ggtcctgaaa	gctttaagct	gaaagctgag	gctggtgatg	ggaaagtcca	tttatectgg	1740
gatgcttcca	gcggagttgt	aggatacagc	gtacagcggg	caacagatga	aaacggccct	1800
ttcactgctg	tagcatccaa	cttgaccgaa	acgtcttata	cggatactaa	cgtgacaaac	1860
ggtacttcat	actattacaa	agtaaccgcc	aaaaccaata	agggatcgag	cgaatccaat	1920
attttgaaaag	cggttccgaa	gatgcctgta	aacggctccg	ctcgctatga	agccgaagaa	1980
ggcacgctga	agggaaacat	tgtggaatcc	agcgggaccg	gctactccgg	tgctggttat	2040
gtaacgaatt	tccacaatcc	aggggattct	ctgacgatga	cgattcaggc	tcccacggca	2100
ggcttgtaca	atcttacaat	cggctaccgt	tctcctcatg	atgacaaaacg	caccaatttc	2160

tcattaaacg gcaaagcggt tggcgaactg ctgcttaaga aaacggctga ttttaaagaa 2220  
 acttccggag gcaaggtgct gttgaatgca ggcgcggaata cgatcagttt tgaaacaggc 2280  
 tggggctggt acgatatcga ctacgtcaga ctggagcctg ccgctgaccg ccacacctcat 2340  
 gcggtaacca aaacgcttac caatccgaat gcgacggtag aagcaaaagc attgatgaac 2400  
 tatctggttg atcaatacgg gaagaatatg ctctctgggtc aagaggaaat aaacgaaatt 2460  
 gattggcttc aagccaatgt aggtaaaaag ccggcgattg cagcgcttga cctgatcgac 2520  
 tattcgccaa gcagagcgga acacggctctt gcatggcact ggaacgcacc gaaaggtctg 2580  
 tgggataagc aaggggggat cgttaccttt gcttctatg cggattcaac cacattcgat 2640  
 atcgatacgc agggaaaaga atgggtggaga ggcttctatg ccgattcaac cacttcgat 2700  
 atagaatatg cgatgaatca tccagagtcc gaagattata aattacttat tcgcgacatc 2760  
 gatgtgattg cagggcaatt gaagaagtgt caggatgcga aggttctgt cctgttccgt 2820  
 cctttgcacg aagcggaagg aaaatggttc tgggtgggag ccaaaggtcc tgagcctgtt 2880  
 aaaaagctgt atattttaat gcacgaccgt ttgacgaatg tgcacaaatt gaacaatctg 2940  
 atttgggtat ggaattctgt tgctccggat tggatccgg gagacgagta tgtggatatt 3000  
 ttgagctttg actcttatcc gcaagcaggt gattacagcc cgcaaatctc aaaatacgaa 3060  
 gaccttgttg cattgggcaa ggacaaaaag ctagtgtcca tgagcgaaaa tggaccgatc 3120  
 ccggaccctg atttgatgaa ggcgatcaaa gctcattgga gctggttcgc tacatggtat 3180  
 ggagattttg tgagagacgg caaacaacac agccttgagc atctgaaaaa agtgtataat 3240  
 catccgaacg tcattacgct ggatgagctc ccaacgaact taaaaacgta tggcattact 3300  
 gagcagccgt ccgtaccggg cagcttcacg ctgaacgctg cgggtgaaac ggcgaaagta 3360  
 tcgctaagct ggacagcatc ggcgaaatgcg aaaagctatg aagtgaagcg ttcgacgact 3420  
 gaaaacggcg cgctcgccac tgtagcgagt gatgtatatg gcagtagcta caccgacaca 3480  
 gctgtaacgg cagatacgac gtaactactc caagtcgtag cgaagaacga tgcaggacag 3540  
 acgctgtcga acacggctag cgcaatgccg aaagcgataa ctcagcagcc gacgacagga 3600  
 ctgctgtctc aatatcgcac agcagatact aaggtgaacg ataatcacct caatccgcaa 3660  
 ttccaaattg taaacaaagg cacaacctcc ataccgatca acgagttgaa aattcgctac 3720  
 tactacacaa tcgacggtga ccgtgagcag actttcaact gcgactatgc gacgctgagc 3780  
 tgctcaaagc tgaacggtaa actggttaaa atggagaagg ctgcaaccgg tgccgattat 3840  
 tatttgaag tcagtttcaa ttcggatgca ggctgttag cacctggagg aagcacgggc 3900  
 gatattccaaa cccgtattca taagacagac tggctgaact ataacgaaag tgacgattat 3960  
 tcgtataaag gcacgcaaac ctcatgtgcc gatcatccta aagttacctt gtatcataac 4020  
 ggctactttg tttggggaac cgagccgaca gctaattaa 4059

<210> 2  
 <211> 1352  
 <212> PRT  
 <213> Paenibacillus polymyxa

<400> 2  
 Met Arg Ala Lys Asn Ser Ser Asn Leu Leu Phe Lys Arg Ser Lys Trp  
 1 5 10 15  
 Leu Pro Val Val Met Ala Cys Thr Met Ile Val Gly Gly Ala Leu Pro  
 20 25 30  
 Ala Pro Ala Val Val His Gly Gln Thr Ala Lys Thr Ile Thr Ile Lys  
 35 40 45  
 Val Asp Thr Phe Lys Asp Arg Lys Pro Ile Ser Pro Tyr Ile Tyr Gly  
 50 55 60  
 Thr Asn Gln Asp Leu Ala Gly Asp Glu Asn Met Ala Ala Arg Arg Leu  
 65 70 75 80  
 Gly Gly Asn Arg Met Thr Gly Tyr Asn Trp Glu Asn Asn Met Ser Asn  
 85 90 95

Ala Gly Ser Asp Trp Gln Gln Ser Ser Asp Asn Tyr Leu Cys Ser Asn  
100 105 110

Gly Gly Leu Thr Gln Ala Glu Cys Glu Lys Pro Gly Ala Val Thr Thr  
115 120 125

Ser Phe His Asp Gln Ser Leu Lys Leu Gly Thr Tyr Ser Leu Val Thr  
130 135 140

Leu Pro Met Ala Gly Tyr Val Ala Lys Asp Gly Asn Gly Ser Val Gln  
145 150 155 160

Glu Ser Glu Lys Ala Pro Ser Ala Arg Trp Asn Gln Val Val Asn Ala  
165 170 175

Lys Asn Ala Pro Phe Gln Leu Gln Pro Asp Leu Asn Asp Asn Arg Val  
180 185 190

Tyr Val Asp Glu Phe Val His Phe Leu Val Asn Lys Tyr Gly Thr Ala  
195 200 205

Ser Thr Lys Ala Gly Val Lys Gly Tyr Ala Leu Asp Asn Glu Pro Ala  
210 215 220

Leu Trp Ser His Thr His Pro Arg Ile His Gly Glu Lys Val Gly Ala  
225 230 235 240

Lys Glu Leu Val Asp Arg Ser Val Ser Leu Ser Lys Ala Val Lys Ala  
245 250 255

Ile Asp Ala Gly Ala Glu Val Phe Gly Pro Val Leu Tyr Gly Phe Gly  
260 265 270

Ala Tyr Lys Asp Leu Gln Thr Ala Pro Asp Trp Asp Ser Val Lys Gly  
275 280 285

Asn Tyr Ser Trp Phe Val Asp Tyr Tyr Leu Asp Gln Met Arg Leu Ser  
290 295 300

Ser Gln Val Glu Gly Lys Arg Leu Leu Asp Val Phe Asp Val His Trp  
305 310 315 320

Tyr Pro Glu Ala Met Gly Gly Gly Ile Arg Ile Thr Asn Glu Val Gly  
325 330 335

Asn Asp Glu Thr Lys Lys Ala Arg Met Gln Ala Pro Arg Thr Leu Trp  
340 345 350

Asp Pro Thr Tyr Lys Glu Asp Ser Trp Ile Ala Gln Trp Asn Ser Glu  
355 360 365

Phe Leu Pro Ile Leu Pro Arg Leu Lys Gln Ser Val Asp Lys Tyr Tyr  
370 375 380

Pro Gly Thr Lys Leu Ala Met Thr Glu Tyr Ser Tyr Gly Gly Glu Asn  
385 390 395 400

Asp Ile Ser Gly Gly Ile Ala Met Thr Asp Val Leu Gly Ile Leu Gly  
 405 410 415  
 Lys Asn Asp Val Tyr Met Ala Asn Tyr Trp Lys Leu Lys Asp Gly Val  
 420 425 430  
 Asn Asn Tyr Val Ser Ala Ala Tyr Lys Leu Tyr Arg Asn Tyr Asp Gly  
 435 440 445  
 Lys Asn Ser Thr Phe Gly Asp Thr Ser Val Ser Ala Gln Thr Ser Asp  
 450 455 460  
 Ile Val Asn Ser Ser Val His Ala Ser Val Thr Asn Ala Ser Asp Lys  
 465 470 475 480  
 Glu Leu His Leu Val Val Met Asn Lys Ser Met Asp Ser Ala Phe Asp  
 485 490 495  
 Ala Gln Phe Asp Leu Ser Gly Ala Lys Thr Tyr Ile Ser Gly Lys Val  
 500 505 510  
 Trp Gly Phe Asp Lys Asn Ser Ser Gln Ile Lys Glu Ala Ala Pro Ile  
 515 520 525  
 Thr Gln Ile Ser Gly Asn Arg Phe Thr Tyr Thr Val Pro Pro Leu Thr  
 530 535 540  
 Ala Tyr His Ile Val Leu Thr Thr Gly Asn Asp Thr Ser Pro Val Glu  
 545 550 555 560  
 Gly Pro Glu Ser Phe Lys Leu Lys Ala Glu Ala Gly Asp Gly Lys Val  
 565 570 575  
 His Leu Ser Trp Asp Ala Ser Ser Gly Val Val Gly Tyr Ser Val Gln  
 580 585 590  
 Arg Ala Thr Asp Glu Asn Gly Pro Phe Thr Ala Val Ala Ser Asn Leu  
 595 600 605  
 Thr Glu Thr Ser Tyr Thr Asp Thr Asn Val Thr Asn Gly Thr Ser Tyr  
 610 615 620  
 Tyr Tyr Lys Val Thr Ala Lys Thr Asn Lys Gly Ser Ser Glu Ser Asn  
 625 630 635 640  
 Ile Leu Lys Ala Val Pro Lys Met Pro Val Asn Gly Pro Ala Arg Tyr  
 645 650 655  
 Glu Ala Glu Glu Gly Thr Leu Lys Gly Thr Ile Val Glu Ser Ser Gly  
 660 665 670  
 Thr Gly Tyr Ser Gly Ala Gly Tyr Val Thr Asn Phe His Asn Pro Gly  
 675 680 685  
 Asp Ser Leu Thr Met Thr Ile Gln Ala Pro Thr Ala Gly Leu Tyr Asn  
 690 695 700

Leu Thr Ile Gly Tyr Arg Ser Pro His Asp Asp Lys Arg Thr Asn Phe  
705 710 715 720

Ser Leu Asn Gly Lys Ala Phe Gly Glu Leu Leu Lys Lys Thr Ala  
725 730 735

Asp Phe Lys Glu Thr Ser Gly Gly Lys Val Leu Leu Asn Ala Gly Ala  
740 745 750

Asn Thr Ile Ser Phe Glu Thr Gly Trp Gly Trp Tyr Asp Ile Asp Tyr  
755 760 765

Val Arg Leu Glu Pro Ala Ala Asp Arg Pro Pro His Ala Val Thr Lys  
770 775 780

Thr Leu Thr Asn Pro Asn Ala Thr Val Glu Ala Lys Ala Leu Met Asn  
785 790 795 800

Tyr Leu Val Asp Gln Tyr Gly Lys Asn Met Leu Ser Gly Gln Glu Glu  
805 810 815

Ile Asn Glu Ile Asp Trp Leu Gln Ala Asn Val Gly Lys Lys Pro Ala  
820 825 830

Ile Ala Ala Leu Asp Leu Ile Asp Tyr Ser Pro Ser Arg Ala Glu His  
835 840 845

Gly Leu Ser Ser Thr Glu Ala Glu Lys Ala Ile Ala Trp Asp Lys Gln  
850 855 860

Gly Gly Ile Val Thr Phe Ala Trp His Trp Asn Ala Pro Lys Gly Leu  
865 870 875 880

Ile Asp Thr Gln Gly Lys Glu Trp Trp Arg Gly Phe Tyr Ala Asp Ser  
885 890 895

Thr Thr Phe Asp Ile Glu Tyr Ala Met Asn His Pro Glu Ser Glu Asp  
900 905 910

Tyr Lys Leu Leu Ile Arg Asp Ile Asp Val Ile Ala Gly Gln Leu Lys  
915 920 925

Lys Leu Gln Asp Ala Lys Val Pro Val Leu Phe Arg Pro Leu His Glu  
930 935 940

Ala Glu Gly Lys Trp Phe Trp Trp Gly Ala Lys Gly Pro Glu Pro Val  
945 950 955 960

Lys Lys Leu Tyr Ile Leu Met His Asp Arg Leu Thr Asn Val His Lys  
965 970 975

Leu Asn Asn Leu Ile Trp Val Trp Asn Ser Val Ala Pro Asp Trp Tyr  
980 985 990

Pro Gly Asp Glu Tyr Val Asp Ile Leu Ser Phe Asp Ser Tyr Pro Gln  
995 1000 1005

Ala Gly Asp Tyr Ser Pro Gln Ile Ser Lys Tyr Glu Asp Leu Val Ala  
 1010 1015 1020  
 Leu Gly Lys Asp Lys Lys Leu Val Ala Met Ser Glu Asn Gly Pro Ile  
 1025 1030 1035 1040  
 Pro Asp Pro Asp Leu Met Lys Ala Tyr Gln Ala His Trp Ser Trp Phe  
 1045 1050 1055  
 Ala Thr Trp Tyr Gly Asp Phe Val Arg Asp Gly Lys Gln Asn Ser Leu  
 1060 1065 1070  
 Glu His Leu Lys Lys Val Tyr Asn His Pro Asn Val Ile Thr Leu Asp  
 1075 1080 1085  
 Glu Leu Pro Thr Asn Leu Lys Thr Tyr Gly Ile Thr Glu Gln Pro Ser  
 1090 1095 1100  
 Val Pro Gly Ser Phe Thr Leu Asn Ala Ala Gly Glu Thr Ala Lys Val  
 1105 1110 1115 1120  
 Ser Leu Ser Trp Thr Ala Ser Ala Asn Ala Lys Ser Tyr Glu Val Lys  
 1125 1130 1135  
 Arg Ser Thr Thr Glu Asn Gly Ala Phe Ala Thr Val Ala Ser Asp Val  
 1140 1145 1150  
 Tyr Gly Ser Ser Tyr Thr Asp Thr Ala Val Thr Ala Asp Thr Thr Tyr  
 1155 1160 1165  
 Tyr Tyr Gln Val Val Ala Lys Asn Asp Ala Gly Gln Thr Leu Ser Asn  
 1170 1175 1180  
 Thr Ala Ser Ala Met Pro Lys Ala Asp Thr Gln Gln Pro Thr Thr Gly  
 1185 1190 1195 1200  
 Leu Leu Leu Gln Tyr Arg Thr Ala Asp Thr Lys Val Asn Asp Asn His  
 1205 1210 1215  
 Leu Asn Pro Gln Phe Gln Ile Val Asn Lys Gly Thr Thr Ser Ile Pro  
 1220 1225 1230  
 Ile Asn Glu Leu Lys Ile Arg Tyr Tyr Thr Thr Ile Asp Gly Asp Arg  
 1235 1240 1245  
 Glu Gln Thr Phe Asn Cys Asp Tyr Ala Thr Leu Ser Cys Ser Lys Leu  
 1250 1255 1260  
 Asn Gly Lys Leu Val Lys Met Glu Lys Ala Ala Thr Gly Ala Asp Tyr  
 1265 1270 1275 1280  
 Tyr Leu Glu Val Ser Phe Asn Ser Asp Ala Gly Val Leu Ala Pro Gly  
 1285 1290 1295  
 Gly Ser Thr Gly Asp Ile Gln Thr Arg Ile His Lys Thr Asp Trp Ser  
 1300 1305 1310

Asn Tyr Asn Glu Ser Asp Asp Tyr Ser Tyr Lys Gly Thr Gln Thr Ser  
1315 1320 1325

Phe Ala Asp His Pro Lys Val Thr Leu Tyr His Asn Gly Val Leu Val  
1330 1335 1340

Trp Gly Thr Glu Pro Thr Ala Asn  
1345 1350

<210> 3

<211> 4056

<212> DNA

<213> Paenibacillus polymyxa

<400> 3

atgaaggcga	aaaatagtag	tagtatttgg	tccaaacggt	ccaaatggct	gcctgtcgtc	60
atggcatgca	cgattatagt	aggggggtgct	ctaccgactc	caactgtagt	tcacgggtcaa	120
acggcaaaga	ctgttaccat	taaagtcgat	acatccaagg	atcgtaagcc	tattagccct	180
tatatattacg	gtacgaatca	ggagttggca	ggcgatgaga	atctgactgc	cagacgactt	240
ggtggcaatc	gaatgaccgg	atataactgg	gaaaacaata	tgtccaatgc	aggaagcgac	300
tggatgcagt	ccagcgatag	ctattttatgc	gacaacgccc	gattgacaaa	agccgaatgt	360
gaaaagccag	gtgcgggtggc	aacctcgttt	cacgatcaat	cgctgaagca	gggcacatat	420
tctttagtc	cactgccgat	ggccggttat	gtggccaagg	atggaaacgg	aagtgtgcag	480
gaaagcgaaa	aggctccttc	cgctcgggtg	aatgaggtcg	taaacgctaa	aatgcgccc	540
tttcaattgc	agcctgatct	gaaagacaat	caggtttatg	cggtgaatt	cgtcaacttt	600
ttagtgaaaa	agtacggcgt	tgcttcaaca	aaaacggggc	tgaaaggata	ctcgctcgac	660
aatgaaccgc	ctctctgggtc	gcatacgc	ccgcgcattc	atggtgaaaa	ggtcggagcg	720
aaagagttgg	tagaccgggtc	ggtaagtta	tccaaagccg	ctaaggcggg	tgacgcgggt	780
gcggaaattt	ttggggcccg	tctttacggg	tttggcgcc	ataaagatct	tcaaactgca	840
cctgattgga	actctgtaaa	aggcaactac	agctgggtcg	tggactatta	cctcgatcaa	900
atgcgcctca	gctcgcaagc	cgaaggcaag	agattgctgg	atgtcttcga	tgtacactgg	960
tatcctgaag	cgatgggcgg	aggcatacga	attacaaatg	aggtaggcaa	cgacgaaacg	1020
aagaaaagcca	gaatgaagc	gcctcgtact	ttgtgggatc	cgacctacaa	ggaagatagc	1080
tggatcgctc	aatggaacag	tgaattcttg	cctttactgc	ctcgattaaa	gcagtcgggtg	1140
gataagtatt	accggggaac	caagctgggt	ttgactgagt	atagctatgg	tggcgaaaaat	1200
gatatttccg	gcggtatcgc	tatggccgat	gtgctgggca	tcttgggcaa	aaacgacggt	1260
tatatggcaa	actactggaa	gttaaaggat	ggtgccaaca	actacgttag	tgccgcttac	1320
aagctttacc	gcaattatga	cggaaaaagc	tctactttcg	gtgatatcag	cgttcatgcg	1380
caaacgtcgg	atattgttaa	tagctcgggtg	catgcttccg	taacggatgc	atcctacaaa	1440
gaactgcacc	tcgttgtcat	gaataaaaagc	atggacagtg	cattcgacgc	ccaatttgat	1500
ctttccggcg	agacgactta	cggttccggg	aaagtatggg	gtttcgacaa	aaatagctcg	1560
caaattaagg	aagcagcgcc	aatcacsc	atttcaggca	accgytttac	ctatacagta	1620
ccgcctttga	cggcttatca	catcgtgttg	actgccggca	atgatacacc	tgtagaaaat	1680
cctgaaagct	ttgcgctgag	ggctgaggct	ggcgatggaa	agtcgattta	tctggacgct	1740
tccagcggag	ttgtaggtta	cagcgtacag	cgggcaacgt	atgaaaacgg	tccttttgct	1800
gctgtagcat	ccaacttggt	cgaaacgtct	tatacggata	cgaacgtaac	gaacggcact	1860
tcttattatt	ataaaataac	cgcaaaaaca	aagacgggaa	cgagcgcac	caatgtcttg	1920
aaagcgggttc	cgcggggcgcc	tgtagacggt	ccggatcgct	atgaagcgga	agatggcacg	1980
ctgaagggga	ccgttgtgga	atccagtggg	accggcttct	ccggtactgg	ttatgtact	2040
aatttccaca	atgcagggga	ttccctgacg	atgacgatcc	aggctccac	ggcaggcttg	2100
tacaatctta	caatcggata	ccgttctcct	catgatgaca	aacgcacgaa	tttctcttta	2160
aatggcaaaag	cgtctggaga	gctggtactt	tggaaaacgg	ctgattttaa	agaaacgtcc	2220
ggtggtaagg	ttctgttgaa	tgcagggg	aatacgcg	gttttgaaac	aggctggggc	2280
tggtatgata	tcgactacgt	caagctggag	ccagctgctg	accgtccacc	gcagtcggta	2340
acgaaaacgc	tcatcaatcc	gaatgcgaca	gtagaagcaa	aagcattgat	gaactacctg	2400

gttgatcaat acggaagaa tatgctttcc ggtcaagagg atatgccga aattgattgg 2460  
 cttcaagcga atgtaggtaa aaagccgget attgcggcac ttgacctgat tgactattcc 2520  
 ccaagcagag cggaacacgg tcttagttcc acagagacgg aaaagggcgat tgaatgggat 2580  
 aagcaagggg gcattgttac ctttgcatgg cactggaacg cgccgaaagg tctgatcgat 2640  
 acgcagggaa aagaatggtg gagaggcttc tatgccgatt cgactacatt cgatatagaa 2700  
 tatgcgatga atcatccaga gtccgaagat tataaattgc ttattcgca catcgatgtg 2760  
 attgcagggc aattgaagaa gttgcaggat gcgaaagtcc ctgtcctgtt ccgtcctttg 2820  
 cacgaagcgg agggcaaag gttctggtgg ggcgctaaag gtcctgagcc tgttaaaaaa 2880  
 ttgtatattt tgatgcacga tctgttgact aatgtgcaca aattgaacaa tctgatctgg 2940  
 gtctggaact ctgttgctcc cgactggtat ccgggagatg agtatgtgga tattttgagc 3000  
 ttcgactctt atccgcaagc aggcgactac agcccgaata ttgcaaaata tgaagacctt 3060  
 gttacattgg gcaaggacaa aaagctagtt tgccatgagc gaaaacggac ctatcccga 3120  
 cccggatctg atgaaggcgt atcaagccca ttggagctgg ttcgctacat ggtatgggga 3180  
 tttcttgaga gacggcaaac aaaacagtcc ttggagcatt tgaaaaaagt gtataatcat 3240  
 ccgaacgtca ttacgcttga aaagctcccg actaacttaa aaacgtatgg cattaccgag 3300  
 caaccgtcag taccgggcag cttcacgctg aacgcagcgg gcgaaacggc gaaagtaaaag 3360  
 ctgagctgga cagcatcagc gaatgcagca agctatgaag tgaagcgctt gacggttgaa 3420  
 aacggcgctg tccgacagc agcgagcgat gtatacggaa gcagctacac cgacacagcc 3480  
 gtaacagcag acacgacgta ctattaccaa gtcgtagcga agaacgatgc aggtcaaacg 3540  
 gtttcgaaca cggctagcgc agcgccgaaa gcggatactc agcagccgac aacgggattg 3600  
 gtgctccagt atcgcacagc ggatacaaat gtgaacgaca atcacttgaa cccgcatttc 3660  
 caaatTTTTaa ataaaggtac aatctccgta ccgatcaacg agttgaaaat tgcgtactac 3720  
 tacacgatcg acggtgaccg tgagcagaca ttcaactgcg actatgcggt gctgagctgc 3780  
 tcgaagctga atggtgaagc ggttaaaatg gataaagctg caaccggtgc tgattattat 3840  
 ttggaagtca gcttcaactc ggtatgcaggc gtgttagcct ctggaggaag cacgggcgga 3900  
 attcaaactc gtattcataa agcagactgg tcgaactata acgaaagtga cgattactcg 3960  
 tataaaggta cgcgacttc attcgacgat catacgaaag ctacgttgta tcacaatggc 4020  
 gtacttggtt ggggaaccga accgacagct aattaa 4056

<210> 4

<211> 1350

<212> PRT

<213> Paenibacillus polymyxa

<400> 4

Met Lys Ala Lys Asn Ser Ser Ser Ile Trp Ser Lys Arg Ser Lys Trp  
 1 5 10 15

Leu Pro Val Val Met Ala Cys Thr Ile Ile Val Gly Gly Ala Leu Pro  
 20 25 30

Thr Pro Thr Val Val His Gly Gln Thr Ala Lys Thr Val Thr Ile Lys  
 35 40 45

Val Asp Thr Ser Lys Asp Arg Lys Pro Ile Ser Pro Tyr Ile Tyr Gly  
 50 55 60

Thr Asn Gln Glu Leu Ala Gly Asp Glu Asn Leu Thr Ala Arg Arg Leu  
 65 70 75 80

Gly Gly Asn Arg Met Thr Gly Tyr Asn Trp Glu Asn Asn Met Ser Asn  
 85 90 95

Ala Gly Ser Asp Trp Met Gln Ser Ser Asp Ser Tyr Leu Cys Asp Asn  
 100 105 110



Ala Gly Leu Thr Lys Ala Glu Cys Glu Lys Pro Gly Ala Val Ala Thr  
115 120 125

Ser Phe His Asp Gln Ser Leu Lys Gln Gly Thr Tyr Ser Leu Val Thr  
130 135 140

Leu Pro Met Ala Gly Tyr Val Ala Lys Asp Gly Asn Gly Ser Val Gln  
145 150 155 160

Glu Ser Glu Lys Ala Pro Ser Ala Arg Trp Asn Glu Val Val Asn Ala  
165 170 175

Lys Asn Ala Pro Phe Gln Leu Gln Pro Asp Leu Lys Asp Asn Gln Val  
180 185 190

Tyr Ala Asp Glu Phe Val Asn Phe Leu Val Lys Lys Tyr Gly Val Ala  
195 200 205

Ser Thr Lys Thr Gly Val Lys Gly Tyr Ser Leu Asp Asn Glu Pro Ala  
210 215 220

Leu Trp Ser His Thr His Pro Arg Ile His Gly Glu Lys Val Gly Ala  
225 230 235 240

Lys Glu Leu Val Asp Arg Ser Val Ser Leu Ser Lys Ala Ala Lys Ala  
245 250 255

Val Asp Ala Gly Ala Glu Ile Phe Gly Pro Val Leu Tyr Gly Phe Gly  
260 265 270

Ala Tyr Lys Asp Leu Gln Thr Ala Pro Asp Trp Asn Ser Val Lys Gly  
275 280 285

Asn Tyr Ser Trp Phe Val Asp Tyr Tyr Leu Asp Gln Met Arg Leu Ser  
290 295 300

Ser Gln Ala Glu Gly Lys Arg Leu Leu Asp Val Phe Asp Val His Trp  
305 310 315 320

Tyr Pro Glu Ala Met Gly Gly Gly Ile Arg Ile Thr Asn Glu Val Gly  
325 330 335

Asn Asp Glu Thr Lys Lys Ala Arg Met Gln Ala Pro Arg Thr Leu Trp  
340 345 350

Asp Pro Thr Tyr Lys Glu Asp Ser Trp Ile Ala Gln Trp Asn Ser Glu  
355 360 365

Phe Leu Pro Leu Leu Pro Arg Leu Lys Gln Ser Val Asp Lys Tyr Tyr  
370 375 380

Pro Gly Thr Lys Leu Ala Leu Thr Glu Tyr Ser Tyr Gly Gly Glu Asn  
385 390 395 400

Asp Ile Ser Gly Gly Ile Ala Met Ala Asp Val Leu Gly Ile Leu Gly  
405 410 415

Lys Asn Asp Val Tyr Met Ala Asn Tyr Trp Lys Leu Lys Asp Gly Ala  
420 425 430

Asn Asn Tyr Val Ser Ala Ala Tyr Lys Leu Tyr Arg Asn Tyr Asp Gly  
435 440 445

Lys Ser Ser Thr Phe Gly Asp Ile Ser Val His Ala Gln Thr Ser Asp  
450 455 460

Ile Val Asn Ser Ser Val His Ala Ser Val Thr Asp Ala Ser Tyr Lys  
465 470 475 480

Glu Leu His Leu Val Val Met Asn Lys Ser Met Asp Ser Ala Phe Asp  
485 490 495

Ala Gln Phe Asp Leu Ser Gly Glu Thr Thr Tyr Gly Ser Gly Lys Val  
500 505 510

Trp Gly Phe Asp Lys Asn Ser Ser Gln Ile Lys Glu Ala Ala Pro Ile  
515 520 525

Thr Gln Ile Ser Gly Asn Arg Phe Thr Tyr Thr Val Pro Pro Leu Thr  
530 535 540

Ala Tyr His Ile Val Leu Thr Ala Gly Asn Asp Thr Pro Val Glu Asn  
545 550 555 560

Pro Glu Ser Phe Ala Leu Arg Ala Glu Ala Gly Asp Gly Lys Ser Ile  
565 570 575

Tyr Leu Asp Ala Ser Ser Gly Val Val Gly Tyr Ser Val Gln Arg Ala  
580 585 590

Thr Tyr Glu Asn Gly Pro Phe Ala Ala Val Ala Ser Asn Leu Val Glu  
595 600 605

Thr Ser Tyr Thr Asp Thr Asn Val Thr Asn Gly Thr Ser Tyr Tyr Tyr  
610 615 620

Lys Ile Thr Ala Lys Thr Lys Thr Gly Thr Ser Ala Ser Asn Val Leu  
625 630 635 640

Lys Ala Val Pro Arg Ala Pro Val Asp Gly Pro Asp Arg Tyr Glu Ala  
645 650 655

Glu Asp Gly Thr Leu Lys Gly Thr Val Val Glu Ser Ser Gly Thr Gly  
660 665 670

Phe Ser Gly Thr Gly Tyr Val Thr Asn Phe His Asn Ala Gly Asp Ser  
675 680 685

Leu Thr Met Thr Ile Gln Ala Pro Thr Ala Gly Leu Tyr Asn Leu Thr  
690 695 700

Ile Gly Tyr Arg Ser Pro His Asp Asp Lys Arg Thr Asn Phe Ser Leu  
705 710 715 720

Asn Gly Lys Ala Ser Gly Glu Leu Val Leu Trp Lys Thr Ala Asp Phe  
 725 730 735  
 Lys Glu Thr Ser Gly Gly Lys Val Leu Leu Asn Ala Gly Ala Asn Thr  
 740 745 750  
 Ile Gly Phe Glu Thr Gly Trp Gly Trp Tyr Asp Ile Asp Tyr Val Lys  
 755 760 765  
 Leu Glu Pro Ala Ala Asp Arg Pro Pro His Ala Val Thr Lys Thr Leu  
 770 775 780  
 Ile Asn Pro Asn Ala Thr Val Glu Ala Lys Ala Leu Met Asn Tyr Leu  
 785 790 795 800  
 Val Asp Gln Tyr Gly Lys Asn Met Leu Ser Gly Gln Glu Asp Met Pro  
 805 810 815  
 Glu Ile Asp Trp Leu Gln Ala Asn Val Gly Lys Lys Pro Ala Ile Ala  
 820 825 830  
 Ala Leu Asp Leu Ile Asp Tyr Ser Pro Ser Arg Ala Glu His Gly Leu  
 835 840 845  
 Ser Ser Thr Glu Thr Glu Lys Ala Ile Glu Trp Asp Lys Gln Gly Gly  
 850 855 860  
 Ile Val Thr Phe Ala Trp His Trp Asn Ala Pro Lys Gly Leu Ile Asp  
 865 870 875 880  
 Thr Gln Gly Lys Glu Trp Trp Arg Gly Phe Tyr Ala Asp Ser Thr Thr  
 885 890 895  
 Phe Asp Ile Glu Tyr Ala Met Asn His Pro Glu Ser Glu Asp Tyr Lys  
 900 905 910  
 Leu Leu Ile Arg Asp Ile Asp Val Ile Ala Gly Gln Leu Lys Lys Leu  
 915 920 925  
 Gln Asp Ala Lys Val Pro Val Leu Phe Arg Pro Leu His Glu Ala Glu  
 930 935 940  
 Gly Lys Trp Phe Trp Trp Gly Ala Lys Gly Pro Glu Pro Val Lys Lys  
 945 950 955 960  
 Leu Tyr Ile Leu Met His Asp Arg Leu Thr Asn Val His Lys Leu Asn  
 965 970 975  
 Asn Leu Ile Trp Val Trp Asn Ser Val Ala Pro Asp Trp Tyr Pro Gly  
 980 985 990  
 Asp Glu Tyr Val Asp Ile Leu Ser Phe Asp Ser Tyr Pro Gln Ala Gly  
 995 1000 1005  
 Asp Tyr Ser Pro Gln Ile Ala Lys Tyr Glu Asp Leu Val Thr Leu Gly  
 1010 1015 1020

Lys Asp Lys Lys Leu Val Cys His Glu Arg Lys Arg Thr Tyr Pro Gly  
1025 1030 1035 1040

Pro Gly Ser Asp Glu Gly Val Ser Ser Pro Leu Glu Leu Val Arg Tyr  
1045 1050 1055

Met Val Trp Gly Phe Leu Glu Arg Arg Gln Thr Lys Gln Ser Leu Glu  
1060 1065 1070

His Leu Lys Lys Val Tyr Asn His Pro Asn Val Ile Thr Leu Glu Lys  
1075 1080 1085

Leu Pro Thr Asn Leu Lys Thr Tyr Gly Ile Thr Glu Gln Pro Ser Val  
1090 1095 1100

Pro Gly Ser Phe Thr Leu Asn Ala Ala Gly Glu Thr Ala Lys Val Lys  
1105 1110 1115 1120

Leu Ser Trp Thr Ala Ser Ala Asn Ala Ala Ser Tyr Glu Val Lys Arg  
1125 1130 1135

Ser Thr Val Glu Asn Gly Ala Phe Ala Thr Val Ala Ser Asp Val Tyr  
1140 1145 1150

Gly Ser Ser Tyr Thr Asp Thr Ala Val Thr Ala Asp Thr Thr Tyr Tyr  
1155 1160 1165

Tyr Gln Val Val Ala Lys Asn Asp Ala Gly Gln Thr Val Ser Asn Thr  
1170 1175 1180

Ala Ser Ala Ala Pro Lys Ala Asp Thr Gln Gln Pro Thr Thr Gly Leu  
1185 1190 1195 1200

Val Leu Gln Tyr Arg Thr Ala Asp Thr Asn Val Asn Asp Asn His Leu  
1205 1210 1215

Asn Pro His Phe Gln Ile Leu Asn Lys Gly Thr Ile Ser Val Pro Ile  
1220 1225 1230

Asn Glu Leu Lys Ile Arg Tyr Tyr Tyr Thr Ile Asp Gly Asp Arg Glu  
1235 1240 1245

Gln Thr Phe Asn Cys Asp Tyr Ala Val Leu Ser Cys Ser Lys Leu Asn  
1250 1255 1260

Gly Lys Leu Val Lys Met Asp Lys Ala Ala Thr Gly Ala Asp Tyr Tyr  
1265 1270 1275 1280

Leu Glu Val Ser Phe Asn Ser Asp Ala Gly Val Leu Ala Ser Gly Gly  
1285 1290 1295

Ser Thr Gly Gly Ile Gln Thr Arg Ile His Lys Ala Asp Trp Ser Asn  
1300 1305 1310

Tyr Asn Glu Ser Asp Asp Tyr Ser Tyr Lys Gly Thr Gln Thr Ser Phe  
1315 1320 1325

Asp Asp His Thr Lys Ala Thr Leu Tyr His Asn Gly Val Leu Val Trp  
 1330 1335 1340

Gly Thr Glu Thr Ala Asn  
 1345 1350

<210> 5  
 <211> 2141  
 <212> DNA  
 <213> Paenibacillus pabuli

<400> 5  
 atgaaggcga aaaatagtag taatatatttg tccaaacgtt ccaaattggct gcctgtcgtc 60  
 atggcatgca cgattatagt agggggggct ctaccggctc caactgtagt tcacgggtcaa 120  
 acggcaaaga ccgttaccat taaagtcgat acatccaagg atcgtaagcc tattagtcct 180  
 tatatatacg gtacgaatca ggatttggca ggcgatgaaa atctggctgc cagacgactt 240  
 ggtggcaatc gaatgaccgg atacaactgg gaaaataata tgtccaatgc gggaagcgat 300  
 tggcagcaat ctagcgataa ctttttatgc aacaatgggt gcctgacaaa agccgaatgt 360  
 gaaaagccgg gagcagtgac gacttcgttt catgatcaat cgctgaagct gggcgcttat 420  
 tcttttagtca cgctgcccgt ggccgggttat gtggccaagg atggaaacgg aagtgtgcag 480  
 gaaagcgaac aggtccttc cgctcggttg aatcaggtcg taaatgccaa aaatgcgccg 540  
 ttccaactac agcctgatct gaatgacaat caggtatatg cggatgaatt cgtcaatttt 600  
 ttagtgaaaa agtacggcgc tgcctcaaca aaggcgggtg tgaaaggata tgcgctcgac 660  
 aatgaacccg ctctctggtc gcatacgcat ccgcgcattc atggtgaaaa agtcnnnnnn 720  
 nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 780  
 nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnni nnttcaaact gcacntgatt 840  
 ggaacttctg taaaaggcaa ctatagctgg ttcgtggact attacctgga tcaaattgctc 900  
 ctcaactcgc aagccgaagg caagagattg ctggatgtat tcgatgtgca ctggtatccc 960  
 gaagcgatgg gcggaggcat acgaattaca aatgaggtag gcaatgacga aacgaagaaa 1020  
 gccagaatgc aggcgcctcg tactttgtgg gacccgacct acaaggaaga tagctggatc 1080  
 gctcaatgga acagcgcatt cttgccttta ctgcctcgat tgaagcagtc ggtggacaag 1140  
 tattaccggg gaaccaagct ggctttgacc gagtataagt acggcggcga aaatgatatt 1200  
 tccggcggta ttgctatgac cgatgtgctg ggcatcttgg gcaaaaacga cgttttatatg 1260  
 gcgaactatt ggaagttaaa ggatgggtgc aacaactacg ttagcgccgc ttacaagctt 1320  
 taccgcaatt atgacggaaa aaacgctact ttcggcgata tcagcggttaa tgcgcaaacy 1380  
 tcggatattg ttaatagctc ggtgcatgct tccgtaacgg atgcaccta caaagaactg 1440  
 cacctcattg tcatgaataa aagcatggac agcgcattcg acgccaatt cgatctttcc 1500  
 ggcgagacga cttacagttc cggtaaaata tggggcttcg ataaaaatag ctcgcaaatt 1560  
 aaggcagtag cgccaatcac gcaaatttca ggcaaccgct ttacctatac agtaccacct 1620  
 ttgacggctt atcacatcgt gttgactgcc gacaatgata cacctgtgcc acctgtggaa 1680  
 gatcctgaaa gctttacgct gagggctgag gctggcgatg ggaaagtcga tttgtcctgg 1740  
 gacgcttcca gcggagttgt ggggttacagt gtacagcggg caacgtatga aaacggtcct 1800  
 tttgctgctg tagcatccaa cttgggtcgaa acgtcttata cggatacgaa cgtaacgaac 1860  
 ggcacttctt actattataa aataaccgca aaaacaaagg cgggaacgag cgaatccaat 1920  
 gtcttgaaag cggttccgcy aacgcctgta gacggcccgg atcgctatga agccgaagat 1980  
 ggcacgctga agggaaccat tgtggaatcc agcgggaccg gcttctccgg tactggttat 2040  
 gtaactaatt tccacaatgc aggggattcc ctgacgatga cgatccacta gtgtcgacct 2100  
 gcaggcgcgc gagctccagc ttttgttccc tttagttagg g 2141

<210> 6  
 <211> 695  
 <212> PRT  
 <213> Paenibacillus pabuli

<400> 6

Met Lys Ala Lys Asn Ser Ser Asn Ile Leu Ser Lys Arg Ser Lys Trp  
 1 5 10 15  
 Leu Pro Val Val Met Ala Cys Thr Ile Ile Val Gly Gly Ala Leu Pro  
 20 25 30  
 Ala Pro Thr Val Val His Gly Gln Thr Ala Lys Thr Val Thr Ile Lys  
 35 40 45  
 Val Asp Thr Ser Lys Asp Arg Lys Pro Ile Ser Pro Tyr Ile Tyr Gly  
 50 55 60  
 Thr Asn Gln Asp Leu Ala Gly Asp Glu Asn Leu Ala Ala Arg Arg Leu  
 65 70 75 80  
 Gly Gly Asn Arg Met Thr Gly Tyr Asn Trp Glu Asn Asn Met Ser Asn  
 85 90 95  
 Ala Gly Ser Asp Trp Gln Gln Ser Ser Asp Asn Phe Leu Cys Asn Asn  
 100 105 110  
 Gly Gly Leu Thr Lys Ala Glu Cys Glu Lys Pro Gly Ala Val Thr Thr  
 115 120 125  
 Ser Phe His Asp Gln Ser Leu Lys Leu Gly Ala Tyr Ser Leu Val Thr  
 130 135 140  
 Leu Pro Met Ala Gly Tyr Val Ala Lys Asp Gly Asn Gly Ser Val Gln  
 145 150 155 160  
 Glu Ser Glu Gln Ala Pro Ser Ala Arg Trp Asn Gln Val Val Asn Ala  
 165 170 175  
 Lys Asn Ala Pro Phe Gln Leu Gln Pro Asp Leu Asn Asp Asn Gln Val  
 180 185 190  
 Tyr Ala Asp Glu Phe Val Asn Phe Leu Val Lys Lys Tyr Gly Ala Ala  
 195 200 205  
 Ser Thr Lys Ala Gly Val Lys Gly Tyr Ala Leu Asp Asn Glu Pro Ala  
 210 215 220  
 Leu Trp Ser His Thr His Pro Arg Ile His Gly Glu Lys Val Xaa Xaa  
 225 230 235 240  
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
 245 250 255  
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
 260 265 270  
 Xaa Xaa Phe Lys Leu His Xaa Ile Gly Thr Ser Val Lys Gly Asn Tyr  
 275 280 285  
 Ser Trp Phe Val Asp Tyr Tyr Leu Asp Gln Met Arg Leu Asn Ser Gln  
 290 295 300

Ala Glu Gly Lys Arg Leu Leu Asp Val Phe Asp Val His Trp Tyr Pro  
 305 310 315 320  
 Glu Ala Met Gly Gly Gly Ile Arg Ile Thr Asn Glu Val Gly Asn Asp  
 325 330 335  
 Glu Thr Lys Lys Ala Arg Met Gln Ala Pro Arg Thr Leu Trp Asp Pro  
 340 345 350  
 Thr Tyr Lys Glu Asp Ser Trp Ile Ala Gln Trp Asn Ser Ala Phe Leu  
 355 360 365  
 Pro Leu Leu Pro Arg Leu Lys Gln Ser Val Asp Lys Tyr Tyr Pro Gly  
 370 375 380  
 Thr Lys Leu Ala Leu Thr Glu Tyr Ser Tyr Gly Gly Glu Asn Asp Ile  
 385 390 395 400  
 Ser Gly Gly Ile Ala Met Thr Asp Val Leu Gly Ile Leu Gly Lys Asn  
 405 410 415  
 Asp Val Tyr Met Ala Asn Tyr Trp Lys Leu Lys Asp Gly Ala Asn Asn  
 420 425 430  
 Tyr Val Ser Ala Ala Tyr Lys Leu Tyr Arg Asn Tyr Asp Gly Lys Asn  
 435 440 445  
 Ala Thr Phe Gly Asp Ile Ser Val Asn Ala Gln Thr Ser Asp Ile Val  
 450 455 460  
 Asn Ser Ser Val His Ala Ser Val Thr Asp Ala Ser Tyr Lys Glu Leu  
 465 470 475 480  
 His Leu Ile Val Met Asn Lys Ser Met Asp Ser Ala Phe Asp Ala Gln  
 485 490 495  
 Phe Asp Leu Ser Gly Glu Thr Thr Tyr Ser Ser Gly Lys Ile Trp Gly  
 500 505 510  
 Phe Asp Lys Asn Ser Ser Gln Ile Lys Ala Val Ala Pro Ile Thr Gln  
 515 520 525  
 Ile Ser Gly Asn Arg Phe Thr Tyr Thr Val Pro Pro Leu Thr Ala Tyr  
 530 535 540  
 His Ile Val Leu Thr Ala Asp Asn Asp Thr Pro Val Pro Pro Val Glu  
 545 550 555 560  
 Asp Pro Glu Ser Phe Thr Leu Arg Ala Glu Ala Gly Asp Gly Lys Val  
 565 570 575  
 Asp Leu Ser Trp Asp Ala Ser Ser Gly Val Val Gly Tyr Ser Val Gln  
 580 585 590  
 Arg Ala Thr Tyr Glu Asn Gly Pro Phe Ala Ala Val Ala Ser Asn Leu  
 595 600 605

